

**IN THE SPECIFICATION:**

Please amend paragraph [0053] as follows: (see next page)

**[0053] Table 1:** list of stress-related genes with identification on the base of homology

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20%amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
a1-1-14.seq	+		SEQ ID NO:1
a1-1-7.seq	+		SEQ ID NO:166
a10-2-12.seq	+		hypothetical protein [Arabidopsis thaliana] (gb AAD08932) SEQ ID NO:2
a10-4-1.seq	+		metallothionein-like protein type 2 Nicotiana plumbaginifolia (gb U35225) SEQ ID NO:3
a10-4-12.seq	+		SEQ ID NO:4
a10-4-15.seq	+		SEQ ID NO:5
a14-1-1.seq	+	=	serine carboxypeptidase-like protein Oryza sativa (dbj BAA04511) SEQ ID NO:6
a14-1-3.seq	+		SEQ ID NO:7
a14-1-4.seq	+		SEQ ID NO:8
a18-1-5.seq	+		EREBP-1 Matricaria chamomilla (dbj BAA87068) SEQ ID NO:9
a18-1-8.seq	+		SEQ ID NO:10
a18-3-2.seq	+		SEQ ID NO:11
a18-3-3.seq	+		EIF-5A (eukaryotic initiation factor 5A2) Solanum tuberosum (sp P56333) SEQ ID NO:12
a18-4-6.seq	+		SEQ ID NO:13
a19-3-1.seq	+		SEQ ID NO:14
a19-3-3.seq	+		SEQ ID NO:15
a19-3-4.seq	+		SEQ ID NO:16
a19-3-9.seq	+		SEQ ID NO:17

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20%amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
a20-1-3.seq	+		SEQ ID NO:18
a3-2-2.seq	-		ribosomal protein L12 (60S) Prunus armeniaca (sp O50003) SEQ ID NO:19
a8-1-1.seq	-		SEQ ID NO:20
a8-1-2.seq	-		geranyl-geranyl reductase chlP-gene <i>Nicotiana tabacum</i> (emb CAA07683) SEQ ID NO:21
a8-1-4.seq	-		early wound inducive gene <i>Nicotiana tabacum</i> (dbj BAA95791) SEQ ID NO:22
a9-1-2.seq	+		epoxide hydrolase <i>Nicotiana tabacum</i> (gb AAB02006) SEQ ID NO:23
a9-3-4.seq	+		immediate-early salicylate-induced glucosyltransferase (IS10a) <i>Nicotiana tabacum</i> (gb U32643) SEQ ID NO:24
a9-4-1.seq	+		SEQ ID NO:25
a9-5-9.seq	+		SEQ ID NO:26
a9-6-11.seq	-		SEQ ID NO:27
a9-7-1.seq	+		SEQ ID NO:28
a9-7-10.seq	+		lipoxxygenase LOX1 <i>Nicotiana tabacum</i> (emb X84040) SEQ ID NO:29
a9-7-11.seq	+		SEQ ID NO:30
c1-1-3.seq	+		SEQ ID NO:31
c1-1-5.seq	+		SEQ ID NO:32
c1-2-2.seq	+		SEQ ID NO:33
c1-3-12.seq	-		SEQ ID NO:34
c10-3-1.seq	-		SEQ ID NO:35

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20%amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
c10-3-5.seq	-		SEQ ID NO:36
c11-2-1.seq	+		SEQ ID NO:37
c11-3-1.seq	+		SEQ ID NO:38
c11-3-3.seq	+		caffeoyl-CoA O-methyltransferase <i>Nicotiana tabacum</i> (emb Z56282) SEQ ID NO:39
c13-1-6.seq	+		SEQ ID NO:40
c13-2-1.seq	+		L19 ribosomal protein <i>Nicotiana tabacum</i> (emb Z31720) SEQ ID NO:41
c13-3-13.seq	+		23S 4.5S rRNA genes chlP-genes <i>Nicotiana tabacum</i> (gb J01446) SEQ ID NO:42
c13-3-6.seq	+		SEQ ID NO:43
c14-1-60.seq	+		glycolate oxidase <i>Lycopersicon esculentum</i> (pir T07032) SEQ ID NO:44
c14-2-10.seq	+		SEQ ID NO:45
c14-2-15.seq	+		ribosomal protein L35-like (60S) <i>Arabidopsis thaliana</i> (emb CAB85998) SEQ ID NO:46
c14-3-4.seq	+		ribosomal protein L23a-like (60S) <i>Arabidopsis thaliana</i> (emb CAB75762) SEQ ID NO:47
c14-5-1.seq	-		predicted protein <i>Oryza sativa</i> (dbj BAA83350) SEQ ID NO:48
c14-6-11.seq	+		predicted protein <i>Arabidopsis thaliana</i> (pir T02387) SEQ ID NO:49
c14-7-4.seq	+		SEQ ID NO:50
c15-1-2.seq	+		SEQ ID NO:51
c15-1-4.seq	+	+	pathogen- and wound-inducible antifungal protein CBP20 precursor <i>Nicotiana tabacum</i> (gb AAB29959) SEQ ID NO:52
c15-11-2.seq	+		SEQ ID NO:53

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20% amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
c15-11-4.seq	+		SEQ ID NO:54
c15-2-8.seq	+		hypothetical protein <i>Arabidopsis thaliana</i> (emb CAB88533) SEQ ID NO:55
c15-3-4.seq	+		hypothetical protein <i>Arabidopsis thaliana</i> (gb AAF63779) SEQ ID NO:56
c15-6-2.seq	+		SEQ ID NO:57
c15-6-3.seq	+		SEQ ID NO:58
c15-7-1.seq	-		SEQ ID NO:59
c15-8-5.seq	-		SEQ ID NO:60
c17-3-1.seq	+		SEQ ID NO:61
c17-3-5.seq	+		SEQ ID NO:62
c17-5-5.seq	+		SEQ ID NO:63
c17-5-8.seq	-		SEQ ID NO:64
c17-6-2.seq	+		SEQ ID NO:65
c18-1-2.seq	+	+	DNAJ protein-like <i>Arabidopsis thaliana</i> (emb CAB86070) SEQ ID NO:66
c18-2-1.seq	+		CCT (chaperonin containing TCP-1) b subunit <i>Oxytricha nova</i> (gb AF188130) SEQ ID NO:67
c19-2-11.seq	+		SEQ ID NO:68
c19-3-10.seq	+		SEQ ID NO:69
c19-4-19.seq	+		SEQ ID NO:70
c19-4-22.seq	+		SEQ ID NO:71
c19-5-1.seq	-		SEQ ID NO:72

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20%amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
c19-5-4.seq	-		SEQ ID NO:73
c19-6-3.seq	+		SEQ ID NO:74
c19-7-4.seq	+		putative translation initiation factor 2B beta subunit (NIFb) EIF2B beta homolog <i>Nicotiana tabacum</i> (gb AF137288) SEQ ID NO:75
c2-1-10.seq	-		SEQ ID NO:76
c2-11-14.seq	+		SEQ ID NO:77
c2-11-2.seq	+		SEQ ID NO:78
c2-2-1.seq	+		SEQ ID NO:79
c2-2-3.seq	+		SEQ ID NO:80
c2-4-1.seq	+		SEQ ID NO:81
c2-5-6.seq	+		SEQ ID NO:82
c2-6-5.seq	-		SEQ ID NO:83
c2-7-1.seq	+		nonsucrose-inducible patatin precursor -strand <i>Solanum brevidens</i> (gb U09331) SEQ ID NO:84
c2-9-14.seq	-		SEQ ID NO:85
c20-1-4.seq	+		DNA- binding protein (pabf) <i>Nicotiana tabacum</i> (gb U06712) SEQ ID NO:86
c3-2-4.seq	+		SEQ ID NO:87
c3-3-6.seq	+		SEQ ID NO:88
c3-4-1.seq	-		SEQ ID NO:89
c4-1-2.seq	+		SEQ ID NO:90

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20%amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
c4-3-3.seq	+		SEQ ID NO:91
c5-1-2.seq	+		SEQ ID NO:92
c6-8-13.seq	+		SEQ ID NO:93
c6-8-4.seq	+		SEQ ID NO:94
c6-8-9.seq	+		SEQ ID NO:95
c7-1-2.seq	-		SEQ ID NO:96
c7-1-6.seq	-		SEQ ID NO:97
c7-3-10.seq	-		SEQ ID NO:98
c7-3-3.seq	-		hypothetical protein <i>Arabidopsis thaliana</i> (emb CAB62623) SEQ ID NO:99
c7-3-9.seq	-		SEQ ID NO:100
c8-1-5.seq	+		SEQ ID NO:101
c9-1-4.seq	+		hypothetical protein <i>Arabidopsis thaliana</i> (dbj BAB08809) SEQ ID NO:102
g10-1-1.seq	+		putative ABA-responsive protein <i>Arabidopsis thaliana</i> (dbj BAB11190) SEQ ID NO:103
g12-1-21.seq	-		hypothetical protein <i>Arabidopsis thaliana</i> (pir T01731) SEQ ID NO:104
g12-1-5.seq	-		Putative membrane-related protein <i>Arabidopsis thaliana</i> (gb AAD38248) SEQ ID NO:105
g14-2-4.seq	+	+	vetispiradiene synthase <i>Solanum tuberosum</i> (gb AAD02223) SEQ ID NO:106
g14-3-10.seq	+		SEQ ID NO:107
g14-3-22.seq	+		hypothetical protein <i>Spinacia oleracea</i> (pir T09217) SEQ ID NO:108
g14-3-3.seq	+		Sequence 162 from Patent EP0953640 <i>Nicotiana tabacum</i> (emb AX014606) SEQ ID NO:109

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20%amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
g14-3-4.seq	+		HR associated Ca2+-binding protein <i>Phaseolus vulgaris</i> (gb AAD47213) SEQ ID NO:110
g14-3-7.seq	+		SEQ ID NO:111
g15-1-37.seq	+		putative golgi transport complex protein <i>Arabidopsis thaliana</i> (gb AAF16568) SEQ ID NO:112
g15-2-2.seq	+	=	ubiquitin <i>Nicotiana tabacum</i> (gb U66264) able to induce HR-like lesions SEQ ID NO:113
g15-3-11.seq	-		Sequence 7 from Patent EP0953640 <i>Nicotiana tabacum</i> (emb AX014451) SEQ ID NO:114
g15-3-7.seq	-		SEQ ID NO:115
g15-4-1.seq	+		SEQ ID NO:116
g17-2-13.seq	+	+	WRKY DNA binding protein <i>Solanum tuberosum</i> (emb CAB97004) SEQ ID NO:117
g17-3-2.seq	+		SEQ ID NO:118
g18-4-7.seq	+		putative ribosomal protein L18 (60S) <i>Arabidopsis thaliana</i> (gb AAF26138) SEQ ID NO:119
g18-5-1.seq	-		SEQ ID NO:120
g18-5-12.seq	-		SEQ ID NO:121
g18-6-12.seq	+		SEQ ID NO:122
g18-6-5.seq	+		SEQ ID NO:123
g18-7-5.seq	+		SEQ ID NO:124
g18-8-7.seq	+		SEQ ID NO:125
g19-1-5.seq	-		unknown protein <i>Arabidopsis thaliana</i> (gb AAF23197) SEQ ID NO:126
g19-1-6.seq	+		SEQ ID NO:127
g19-1-7.seq	+		putative protein <i>Arabidopsis thaliana</i> (emb CAB82697) SEQ ID NO:128



Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20% amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
g19-2-1.seq	+		SEQ ID NO:129
g19-2-9.seq	+		SEQ ID NO:130
g2-1-2.seq	+	+	5-epi-aristolochene synthase <i>Nicotiana tabacum</i> (emb Y08847) SEQ ID NO:131
g20-2-20.seq	+		hypothetical protein <i>Arabidopsis thaliana</i> (gb AAF14679) SEQ ID NO:132
g20-2-29.seq	+		SEQ ID NO:133
g20-2-31.seq	+		SEQ ID NO:134
g3-1-1.seq	+		ankyrin-like protein <i>Arabidopsis thaliana</i> (dbj BAB10271) SEQ ID NO:135
g3-1-4.seq	+	=	ADP-ribosylation factor <i>Capsicum annuum</i> (gb AAF65512) SEQ ID NO:136
g6-2-13.seq	+	+	leucoanthocyanidin dioxygenase 2, putative; 51024-52213 <i>Arabidopsis thaliana</i> (gb AAG21532) SEQ ID NO:137
g6-3-7.seq	+	+	ATP citrate lyase <i>Arabidopsis thaliana</i> (dbj BAB09916) SEQ ID NO:138
g6-4-4.seq	+		SEQ ID NO:139
g6-4-5.seq	+		ATP-dependent protease proteolytic subunit ClpP-like protein <i>Arabidopsis thaliana</i> (dbj BAB09831) SEQ ID NO:140
g7-1-1.seq	+		RNA-binding protein MEI2 (meiotic regulator), putative; 36123-32976 <i>Arabidopsis thaliana</i> (gb AAG12640) SEQ ID NO:141
g7-1-4.seq	+		SEQ ID NO:142
g9-2-2.seq	+	+	P-glycoprotein-like protein <i>Arabidopsis thaliana</i> (emb CAB71875) SEQ ID NO:143
g9-2-6.seq	+		SEQ ID NO:144
g9-3-17.seq	+		SEQ ID NO:145

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20% amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
g9-3-4.seq	+		SEQ ID NO:146
g9-5-5.seq	+		SEQ ID NO:147
g9-6-1.seq	+	+	lipoxigenase <i>Solanum tuberosum</i> (gb AAD09202) SEQ ID NO:148
t12-1-7.seq	+	+	serine/threonine/tyrosine-specific protein kinase APK1A <i>Arabidopsis thaliana</i> (sp Q06548) SEQ ID NO:149
t12-2-1.seq	+		chitinase class 4 <i>Vigna unguiculata</i> (pir S57476) SEQ ID NO:150
t12-2-18.seq	+		SEQ ID NO:151
t18-2-5.seq	+	+	basic PRB-1b <i>Nicotiana tabacum</i> (emb X66942) SEQ ID NO:152
t18-3-2.seq	+		SEQ ID NO:153
t18-3-6.seq	+		RNA- or ssDNA-binding protein <i>Vicia faba</i> (pir T12196) SEQ ID NO:154
t18-4-18.seq	-		ADP-glucose pyrophosphorylase small subunit <i>Solanum tuberosum</i> (emb X55650) SEQ ID NO:155
t2-1-1-1.seq	+		ubiquitin carrier protein <i>Lycopersicon esculentum</i> (sp P35135) SEQ ID NO:156
t2-1-3.seq	+		Hypothetical protein chlP <i>Nicotiana tabacum</i> (sp P12204) SEQ ID NO:157
t2-6-3.seq	+		SEQ ID NO:158
t7-1-12.seq	+	=	Hypothetical protein <i>Arabidopsis thaliana</i> (gb AAF26468) SEQ ID NO:159
t7-1-14.seq	+		t7-2-4.seq + intron SEQ ID NO:167
t7-2-4.seq	+	+	Multifunctional protein of glyoxysomal fatty acid beta-oxidation <i>Brassica napus</i> (emb AJ000886) SEQ ID NO:164, 160

Clone number	DD+/-	N+/-/=	homology E<10-3 with at least 20%amino acids or 50% nucleic acids identical nonredundant DNA and protein sequence databases (blastx/blastn)
t7-4-7.seq	+		putative glutathione S-transferase; 80986-80207 <i>Arabidopsis thaliana</i> (gb AAF15930) SEQ ID NO:161
t7-4-8.seq	+		SEQ ID NO:162
t7-5-4.seq	+		SEQ ID NO:163
t7-5-5.seq	+		SEQ ID NO:164
t7-6-4.seq	+		SEQ ID NO:165

DD+ = induced on differential display gel

DD- = repressed on differential display gel

N+ = induced on Northern

N- = repressed on Northern

N= = constant on Northern

All GenBank, or other databases, references cited herein are hereby incorporated by reference to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.